

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/417,174DATE: 08/03/95
TIME: 09:19:21

INPUT SET: S5188.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

- (i) APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG, STEVEN A.
- (ii) TITLE OF INVENTION: MELANOMA ANTIGENS AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
- (iii) NUMBER OF SEQUENCES: 126
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 - (B) STREET: 345 PARK AVENUE
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: USA
 - (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: ASCII
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/08/417,174
 - (B) FILING DATE: 05-APR-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/08/231,565
 - (B) FILING DATE: 22-APR-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CAROL M. GRUPPI
 - (B) REGISTRATION NUMBER: 37,341
 - (C) REFERENCE/DOCKET NUMBER: 2026-4124US1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 758-4800
 - (B) TELEFAX: (212) 751-6849
 - (C) TELEX: 421792

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/417,174DATE: 08/03/95
TIME: 09:19:26

INPUT SET: S5188.raw

47 (2) INFORMATION FOR SEQ ID NO: 1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1559

51 (B) TYPE: NUCLEOTIDE

52 (C) STRANDEDNESS: DOUBLE

53 (D) TOPOLOGY: UNKNOWN
54
55
56
57
58
5960 (ii) MOLECULE TYPE: cDNA
6162 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63

64	AGCAGACAGA GGACTCTCAT TAAGGAAGGT GTCCTGTGCC	40
65		
66	CTGACCCTAC AAGATGCCAA GAGAAGATGC TCACTTCATC	80
67		
68	TATGGTTACC CCAAGAAGGG GCACGGCCAC TCTTACACCA	120
69		
70	CGGCTGAAGA GGCCGCTGGG ATCGGCATCC TGACAGTGAT	160
71		
72	CCTGGGAGTC TTA CTGCTCA TCGGCTGTTG GTATTGTAGA	200
73		
74	AGACGAAATG GATACAGAGC CTTGATGGAT AAAAGTCTTC	240
75		
76	ATGTTGGCAC TCAATGTGCC TTAACAAGAA GATGCCCACA	280
77		
78	AGAAGGGTTT GATCATCGGG ACAGCAAAGT GTCTCTTCAA	320
79		
80	GAGAAAAACT GTGAACCTGT GGTTCCTCAAT GCTCCACCTG	360
81		
82	CTTATGAGAA ACTCTCTGCA GAACAGTCAC CACCACCTTA	400
83		
84	TTCACCTTAA GAGCCAGCGA GACACCTGAG ACATGCTGAA	440
85		
86	ATTATTTCTC TCACACTTTT GCTTGAATTT AATACAGACA	480
87		
88	TCTAATGTTT TCCTTTGGAA TGGTGTAGGA AAAATGCAAG	520
89		
90	CCATCTCTAA TAATAAGTCA GTGTTAAAAAT TTTAGTAGGT	560
91		
92	CCGCTAGCAG TACTAATCAT GTGAGGAAAT GATGAGAAAT	600
93		
94	ATTAAATTGG GAAAACTCCA TCAATAAATG TTGCAATGCA	640
95		
96	TGATACTATC TGTGCCAGAG GTAATGTTAG TAAATCCATG	680
97		
98	GTGTTATTTT CTGAGAGACA GAATTCAAGT GGGTATTCTG	720
99		

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/417,174DATE: 08/03/95
TIME: 09:19:31

INPUT SET: S5188.raw

100	GGGCCATCCA ATTTCTCTTT ACTTGAAATT TGGCTAATAA	760
101		
102	CAAAC TAGTC AGGTTTTCGA ACCTTGACCG ACATGAACTG	800
103		
104	TACACAGAAT TGTTCAGTA CTATGGAGTG CTCACAAAGG	840
105		
106	ATACTTTTAC AGGTTAAGAC AAAGGGTTGA CTGGCCTATT	880
107		
108	TATCTGATCA AGAACATGTC AGCAATGTCT CTTTGTGCTC	920
109		
110	TAAAATTCTA TTATACTACA ATAATATATT GTAAAGATCC	960
111		
112	TATAGCTCTT TTTTTTTGAG ATGGAGTTTC GCTTTTGTTG	1000
113		
114		
115		
116		
117		
118		
119	CCCAGGCTGG AGTGCAATGG CGCGATCTTG GCTCACCATA	1040
120		
121	ACCTCCGCCT CCCAGGTTCA AGCAATTCTC CTGCCTTAGC	1080
122		
123	CTCCTGAGTA GCTGGGATTA CAGGCGTGCG CCACTATGCC	1120
124		
125	TGACTAATTT TGTAGTTTTA GTAGAGACGG GGTTCCTCCA	1160
126		
127	TGTTGGTCAG GCTGGTCTCA AACTCCTGAC CTCAGGTGAT	1200
128		
129	CTGCCCCGCT CAGCCTCCCA AAGTGCTGGA ATTACAGGCG	1240
130		
131	TGAGCCACCA CGCCTGGCTG GATCCTATAT CTTAGGTAAG	1280
132		
133	ACATATAACG CAGTCTAATT ACATTTCACT TCAAGGCTCA	1320
134		
135	ATGCTATTCT AACTAATGAC AAGTATTTTC TACTAAACCA	1360
136		
137	GAAATTGGTA GAAGGATTTA AATAAGTAAA AGCTACTATG	1400
138		
139	TACTGCCTTA GTGCTGATGC CTGTGTACTG CCTTAAATGT	1440
140		
141	ACCTATGGCA ATTTAGCTCT CTTGGGTTCC CAAATCCCTC	1480
142		
143	TCACAAGAAT GTGCAGAAGA AATCATAAAG GATCAGAGAT	1520
144		
145	TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1559
146		
147		

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118

(B) TYPE: amino acid

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/417,174DATE: 08/03/95
TIME: 09:19:36

INPUT SET: S5188.raw

153 (C) STRANDEDNESS: Unknown
154 (D) TOPOLOGY: Unknown
155
156 (ii) MOLECULE TYPE: Protein
157
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
159
160 Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys
161 1 5 10
162 Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala
163 15 20 25
164 Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu
165 30 35 40
166 Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
167 45 50 55
168 Leu Met Asp Lys Ser Leu His Val Gly Thr Gln Cys Ala Leu
169 60 65 70
170 Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp His Arg Asp Ser
171 75 80
172
173
174
175
176
177
178 Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val Val Pro
179 85 90 95
180 Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
181 100 105 110
182 Pro Pro Pro Tyr Ser Pro
183 115
184
185
186 (2) INFORMATION FOR SEQ ID NO: 3:
187
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 9
190 (B) TYPE: amino acid
191 (C) STRANDEDNESS: Unknown
192 (D) TOPOLOGY: Unknown
193
194 (ii) MOLECULE TYPE: Peptide
195
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
197
198
199 Thr Thr Ala Glu Glu Ala Ala Gly Ile
200 1 5
201
202
203 (2) INFORMATION FOR SEQ ID NO: 4:
204
205 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/417,174DATE: 08/03/95
TIME: 09:19:41

INPUT SET: S5188.raw

206 (A) LENGTH: 9
207 (B) TYPE: amino acid
208 (C) STRANDEDNESS: Unknown
209 (D) TOPOLOGY: Unknown
210
211 (ii) MOLECULE TYPE: Peptide
212
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
214
215
216 Ala Ala Gly Ile Gly Ile Leu Thr Val
217 1 5
218
219
220 (2) INFORMATION FOR SEQ ID NO: 5:
221
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 9
224 (B) TYPE: amino acid
225 (C) STRANDEDNESS: Unknown
226 (D) TOPOLOGY: Unknown
227
228 (ii) MOLECULE TYPE: Peptide
229
230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
231
232
233
234
235
236
237 Gly Ile Gly Ile Leu Thr Val Ile Leu
238 1 5
239
240
241 (2) INFORMATION FOR SEQ ID NO: 6:
242
243 (i) SEQUENCE CHARACTERISTICS:
244 (A) LENGTH: 9
245 (B) TYPE: amino acid
246 (C) STRANDEDNESS: Unknown
247 (D) TOPOLOGY: Unknown
248
249 (ii) MOLECULE TYPE: Peptide
250
251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
252
253
254 Gly Ile Leu Thr Val Ile Leu Gly Val
255 1 5
256
257
258 (2) INFORMATION FOR SEQ ID NO: 7:

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/417,174

DATE: 08/03/95
TIME: 09:19:47

INPUT SET: S5188.raw

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Original Text